

Attorney Docket No. 5470-130DV

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: French et al.

Serial No.: 09/497,822

Filed: February 3, 2000

Confirmation No. 7943

Group Art Unit: 1646

Examiner: M. Pak

For: ANDROGEN RECEPTOR PROTEINS, RECOMBINANT DNA MOLECULES
CODING FOR SUCH, AND USE OF SUCH COMPOSITIONS

Date: November 26, 2002

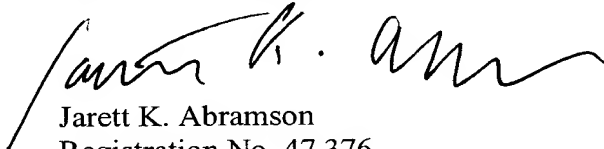
Commissioner for Patents
Washington, DC 20231

**STATEMENT IN SUPPORT OF FILING A
SEQUENCE LISTING UNDER 37 CFR § 1.821(f)**

Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence listing are the same. I also hereby state as required by 37 CFR § 1.821(h) that the computer readable copy submitted concurrently herewith contains no new matter, nor does it go beyond the disclosure of the application as filed.

Respectfully submitted,


Jarett K. Abramson

Registration No. 47,376

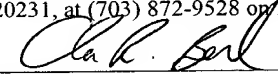


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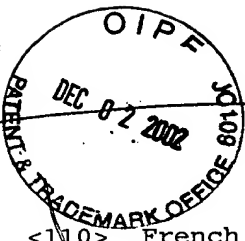
PATENT TRADEMARK OFFICE

CERTIFICATE OF FACSIMILE TRANSMISSION

I hereby certify that this correspondence is being sent by facsimile transmission to Commissioner for Patents, Washington, DC 20231, at (703) 872-9528 on November 26, 2002.


Clara R. Beard

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DEC 05 2002
TECH CENTER 1600/2900



SEQUENCE LISTING

<110> French, Frank
Wilson, Elizabeth
Joseph, David
Lubahn, Dennis

<120> ANDROGEN RECEPTOR PROTEINS RECOMBINANT DNA MOLECULES AND CODING
FOR SUCH AND USE OF SUCH COMPOSITIONS

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<140> US 09/497,822

<141> 2000-02-03

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<170> PatentIn version 3.1

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DEC 05 2002
TECH CENTER 1600/2900

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Gly Met
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Met Val Tyr Thr Cys His Arg Asp Lys Asn Cys Ile Ile Asn Lys Val
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| ggctgagggt | tcctagagca | aatggcacaa | tgccacgagg | ccgatctat | ccctatgacg | 240 |
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| gaa gtg atc cag aac ccg ggc ccc agg cac cca gag gcc gcg agc gca | 2004 |
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| Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp | |
| 145 150 155 | |
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| Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly | |
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| tta agc agc tgc tcc gct gac ctt aaa gac atc ctg agc gag gcc agc | 2436 |
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| 180 185 190 | |
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| Thr Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly | |
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| agc agc agc ggg aga gcg agg gag gcc tcg ggg gct ccc act tcc tcc | 2532 |
| Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser | |
| 210 215 220 | |
| aag gac aat tac tta ggg ggc act tcg acc att tct gac aac gcc aag | 2580 |
| Lys Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys | |
| 225 230 235 | |
| gag ttg tgt aag gca gtg tcg gtg tcc atg ggc ctg ggt gtg gag gcg | 2628 |

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| ttg | gag | cat | ctg | agt | cca | ggg | gaa | cag | ctt | cgg | ggg | gat | tgc | atg | tac | | 2676 |
| Leu | Glu | His | Leu | Ser | Pro | Gly | Glu | Gln | Leu | Arg | Gly | Asp | Cys | Met | Tyr | | |
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| Ser | Thr | Glu | Asp | Thr | Ala | Glu | Tyr | Ser | Pro | Phe | Lys | Gly | Gly | Tyr | Thr | | |
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| aaa | ggg | cta | gaa | ggc | gag | agc | cta | ggc | tgc | tct | ggc | agc | gct | gca | gca | | 2868 |
| Lys | Gly | Leu | Glu | Gly | Glu | Ser | Leu | Gly | Cys | Ser | Gly | Ser | Ala | Ala | Ala | | |
| 320 | | | | | 325 | | | | 330 | | | | | 335 | | | |
| ggg | agc | tcc | ggg | aca | ctt | gaa | ctg | ccg | tct | acc | ctg | tct | ctc | tac | aag | | 2916 |
| Gly | Ser | Ser | Gly | Thr | Leu | Glu | Leu | Pro | Ser | Thr | Leu | Ser | Leu | Tyr | Lys | | |
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| | 385 | | | | | 390 | | | | | 395 | | | | | | |
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| Leu | His | Gly | Ala | Gly | Ala | Ala | Gly | Pro | Gly | Ser | Gly | Ser | Pro | Ser | Ala | | |
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| Ala | Ala | Ser | Ser | Ser | Trp | His | Thr | Leu | Phe | Thr | Ala | Glu | Glu | Gly | Gln | | |
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| Leu | Tyr | Gly | Pro | Cys | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | | |
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| Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Glu | Ala | Gly | | |
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| gct | gta | gcc | ccc | tac | ggc | tac | act | cgg | ccc | cct | cag | ggg | ctg | gcg | ggc | | 3348 |
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| cag gaa agc gac ttc acc gca cct gat gtg tgg tac cct ggc ggc atg Gln Glu Ser Asp Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met 500 505 510 | | | | 3396 |
| gtg agc aga gtg ccc tat ccc agt ccc act tgt gtc aaa agc gaa atg Val Ser Arg Val Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met 515 520 525 | | | | 3444 |
| ggc ccc tgg atg gat agc tac tcc gga cct tac ggg gac atg cgt ttg Gly Pro Trp Met Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu 530 535 540 | | | | 3492 |
| gag act gcc agg gac cat gtt ttg ccc att gac tat tac ttt cca ccc Glu Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro 545 550 555 | | | | 3540 |
| cag aag acc tgc ctg atc tgt gga gat gaa gct tct ggg tgt cac tat Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr 560 565 570 575 | | | | 3588 |
| gga gct ctc aca tgt gga agc tgc aag gtc ttc ttc aaa aga gcc gct Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala 580 585 590 | | | | 3636 |
| gaa ggg aaa cag aag tac ctg tgc gcc agc aga aat gat tgc act att Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile 595 600 605 | | | | 3684 |
| gat aaa ttc cga agg aaa aat tgt cca tct tgt cgt ctt cgg aaa tgt Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys 610 615 620 | | | | 3732 |
| tat gaa gca ggg atg act ctg gga gcc cgg aag ctg aag aaa ctt ggt Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly 625 630 635 | | | | 3780 |
| aat ctg aaa cta cag gag gaa gga gag gct tcc agc acc acc agc ccc Asn Leu Lys Leu Gln Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro 640 645 650 655 | | | | 3828 |
| act gag gag aca acc cag aag ctg aca gtg tca cac att gaa ggc tat Thr Glu Glu Thr Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr 660 665 670 | | | | 3876 |
| gaa tgt cag ccc atc ttt ctg aat gtc ctg gaa gcc att gag cca ggt Glu Cys Gln Pro Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly 675 680 685 | | | | 3924 |
| gta gtg tgt gct gga cac gac aac aac cag ccc gac tcc ttt gca gcc Val Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala 690 695 700 | | | | 3972 |
| ttg ctc tct agc ctc aat gaa ctg gga gag aga cag ctt gta cac gtg Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val 705 710 715 | | | | 4020 |
| gtc aag tgg gcc aag gcc ttg cct ggc ttc cgc aac tta cac gtg gac Val Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp 720 725 730 735 | | | | 4068 |

D/
Cont

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| gcc atg ggc tgg cga tcc ttc acc aat gtc aac tcc agg atg ctc tac Ala Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr 755 760 765 | 4164 |
| ttc gcc cct gat ctg gtt ttc aat gag tac cgc atg cac aag tcc cgg Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg 770 775 780 | 4212 |
| atg tac agc cag tgt gtc cga atg agg cac ctc tct caa gag ttt gga Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly 785 790 795 | 4260 |
| tgg ctc caa atc acc ccc cag gaa ttc ctg tgc atg aaa gca ctg cta Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu 800 805 810 815 | 4308 |
| ctc ttc agc att att cca gtg gat ggg ctg aaa aat caa aaa ttc ttt Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe 820 825 830 | 4356 |
| gat gaa ctt cga atg aac tac atc aag gaa ctc gat cgt atc att gca Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala 835 840 845 | 4404 |
| tgc aaa aga aaa aat ccc aca tcc tgc tca aga cgc ttc tac cag ctc Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu 850 855 860 | 4452 |
| acc aag ctc ctg gac tcc gtg cag cct att gcg aga gag ctg cat cag Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln 865 870 875 | 4500 |
| ttc act ttt gac ctg cta atc aag tca cac atg gtg agc gtg gac ttt Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe 880 885 890 895 | 4548 |
| ccg gaa atg atg gca gag atc atc tct gtg caa gtg ccc aag atc ctt Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu 900 905 910 | 4596 |
| tct ggg aaa gtc aag ccc atc tat ttc cac acc cag tgaagcattg Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln 915 920 | 4642 |
| gaaaccctat ttccccaccc cagctcatgc cccctttcag atgtcttctg cctgttataa | 4702 |
| ctctgcacta ctctctgca gtgccttggg gaatttctc tattgatgta cagtctgtca | 4762 |
| tgaacatggt cctgaattct atttgctggg cttttttttt ctctttctct cctttctttt | 4822 |
| tcttttccc tccctatcta accctcccat ggcaccttca gactttgctt cccattgtgg | 4882 |
| ctcttatctg tgttttgaat ggtgttgtat gcctttaaat ctgtgatgat cctcatatgg | 4942 |
| cccagtgtca agttgtgctt gtttacagca ctactctgtg ccagccacac aaacgtttac | 5002 |

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Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
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Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
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Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp
85 90 95

Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu
100 105 110

Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His
115 120 125

Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser
130 135 140

Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser
145 150 155 160

Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu
165 170 175

Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr
180 185 190

Met Gln Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser
195 200 205

Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys
210 215 220

Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu
225 230 235 240

Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu
245 250 255

Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala
260 265 270

Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro
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Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser
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Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys
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Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly
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Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser
340 345 350

Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn
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Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro His
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Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala
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Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu
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His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala
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Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu
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Tyr Gly Pro Cys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
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Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala

DI
Cont

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Glu Ser Asp Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val
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Ser Arg Val Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly
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Pro Trp Met Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu
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Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln
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Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly
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Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu
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Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp
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Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr
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Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn
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Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr
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Glu Glu Thr Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu
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Cys Gln Pro Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val
 675 680 685

Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu
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Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val
 705 710 715 720

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Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp
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740 745 750

Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe
755 760 765

Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met
770 775 780

Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp
785 790 795 800

Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu
805 810 815

Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp
820 825 830

Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys
835 840 845

Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr
850 855 860

Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe
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Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro
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Met Glu Val Gln
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tta ggg ctg gga agg gtc tac cca cgg ccc ccg tcc aag acc tat cga 1182
Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser Lys Thr Tyr Arg
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gga gcg ttc cag aat ctg ttc cag agc gtg cgc gaa gcg atc cag aac 1230
Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu Ala Ile Gln Asn
25 30 35
ccg ggc ccc agg cac cct gag gcc gct agc ata gca cct ccc ggt gcc 1278
Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile Ala Pro Pro Gly Ala
40 45 50
tgt tta cag cag cgg cag gag act agc ccc cgg cgg cgg cgg cgg cag 1326
Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg Arg Arg Arg Gln
55 60 65

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| gcc tcc gag ggc cac cct gag agc ggc tgc ctc ccg gag cct gga gct Ala Ser Glu Gly His Pro Glu Ser Gly Cys Leu Pro Glu Pro Gly Ala 105 110 115 | 1470 |
| gcc acg gct cct ggc aag ggg ctg ccg cag cag cca cca gct cct cca Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro Pro Ala Pro Pro 120 125 130 | 1518 |
| gat cag gat gac tca gct gcc cca tcc acg ttg tcc cta ctg ggc ccc Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro 135 140 145 | 1566 |
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| agc gag gcc ggc acc atg caa ctt ctt cag cag cag cag caa cag caa Ser Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln Gln Gln Gln 165 170 175 180 | 1662 |
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| gct ccc tct tcc tcc aag gat agt tac cta ggg ggc aat tcg acc ata Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr Ile 215 220 225 | 1806 |
| tct gac agt gcc aag gag ttg tgt aaa gca gtg tct gtg tcc atg ggg Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly 230 235 240 | 1854 |
| ttg ggt gtg gaa gca ctg gaa cat ctg agt cca ggg gag cag ctt cgg Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu Arg 245 250 255 260 | 1902 |
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| ccc act cct tgt gcg cct ctg gcc gaa tgc aaa ggt ctt tcc ctg gac Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly Leu Ser Leu Asp 280 285 290 | 1998 |
| gaa ggc ccg ggc aaa ggc act gaa gag act gct gag tat tcc tct ttc Glu Gly Pro Gly Lys Gly Thr Glu Glu Thr Ala Glu Tyr Ser Ser Phe 295 300 305 | 2046 |
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D1
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| ggc | agc | agt | gaa | gca | ggc | agc | tct | ggg | aca | ctt | gag | atc | ccg | tcc | tca | 2142 | |
| Gly | Ser | Ser | Glu | Ala | Gly | Ser | Ser | Gly | Thr | Leu | Glu | Ile | Pro | Ser | Ser | | |
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| ctg | tct | ctg | tat | aag | tct | gga | gca | gta | gac | gag | gca | gca | gca | tac | cag | 2190 | |
| Leu | Ser | Leu | Tyr | Lys | Ser | Gly | Ala | Val | Asp | Glu | Ala | Ala | Ala | Tyr | Gln | | |
| | | | | 345 | | | | | 350 | | | | | 355 | | | |
| aat | cgc | gac | tac | tac | aac | ttt | ccg | ctc | gct | ctg | tcc | ggg | ccg | ccg | cac | 2238 | |
| Asn | Arg | Asp | Tyr | Tyr | Asn | Phe | Pro | Leu | Ala | Leu | Ser | Gly | Pro | Pro | His | | |
| | | | 360 | | | | | 365 | | | | | 370 | | | | |
| ccc | ccg | ccc | cct | acc | cat | cca | cac | gcc | cgc | atc | aag | ctg | gag | aac | ccg | 2286 | |
| Pro | Pro | Pro | Pro | Thr | His | Pro | His | Ala | Arg | Ile | Lys | Leu | Glu | Asn | Pro | | |
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| tcg | gac | tac | ggc | agc | gcc | tgg | gct | gcg | gcg | gca | gcg | caa | tgc | cgc | tat | 2334 | |
| Ser | Asp | Tyr | Gly | Ser | Ala | Trp | Ala | Ala | Ala | Ala | Ala | Gln | Cys | Arg | Tyr | | |
| | 390 | | | | | 395 | | | | | 400 | | | | | | |
| ggg | gac | ttg | gct | agc | cta | cat | gga | ggg | agt | gta | gcc | gga | ccc | agc | act | 2382 | |
| Gly | Asp | Leu | Ala | Ser | Leu | His | Gly | Gly | Ser | Val | Ala | Gly | Pro | Ser | Thr | | |
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| gga | tcg | ccc | cca | gcc | acc | gcc | tct | tct | tcc | tgg | cat | act | ctc | ttc | aca | 2430 | |
| Gly | Ser | Pro | Pro | Ala | Thr | Ala | Ser | Ser | Ser | Trp | His | Thr | Leu | Phe | Thr | | |
| | | | | 425 | | | | | 430 | | | | | 435 | | | |
| gct | gaa | gaa | ggc | caa | tta | tat | ggg | cca | gga | ggc | ggg | ggc | ggc | agc | agt | 2478 | |
| Ala | Glu | Glu | Gly | Gln | Leu | Tyr | Gly | Pro | Gly | Gly | Gly | Gly | Gly | Ser | Ser | | |
| | | | 440 | | | | | 445 | | | | | 450 | | | | |
| agc | cca | agc | gat | gct | ggg | cct | gta | gcc | ccc | tat | ggc | tac | act | cgg | ccc | 2526 | |
| Ser | Pro | Ser | Asp | Ala | Gly | Pro | Val | Ala | Pro | Tyr | Gly | Tyr | Thr | Arg | Pro | | |
| | | | 455 | | | | 460 | | | | | 465 | | | | | |
| cct | cag | ggg | ctg | gca | agc | cag | gag | ggt | gac | ttc | tct | gcc | tct | gaa | gtg | 2574 | |
| Pro | Gln | Gly | Leu | Ala | Ser | Gln | Glu | Gly | Asp | Phe | Ser | Ala | Ser | Glu | Val | | |
| | 470 | | | | | 475 | | | | | 480 | | | | | | |
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| Trp | Tyr | Pro | Gly | Gly | Val | Val | Asn | Arg | Val | Pro | Tyr | Pro | Ser | Pro | Ser | | |
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| tgt | gtt | aaa | agt | gaa | atg | gga | cct | tgg | atg | gag | aac | tac | tcc | gga | cct | 2670 | |
| Cys | Val | Lys | Ser | Glu | Met | Gly | Pro | Trp | Met | Glu | Asn | Tyr | Ser | Gly | Pro | | |
| | | | | 505 | | | | | 510 | | | | | 515 | | | |
| tat | ggg | gac | atg | cgt | ttg | gac | agt | acc | agg | gac | cac | gtt | tta | ccc | atc | 2718 | |
| Tyr | Gly | Asp | Met | Arg | Leu | Asp | Ser | Thr | Arg | Asp | His | Val | Leu | Pro | Ile | | |
| | | | | 520 | | | | 525 | | | | | 530 | | | | |
| gac | tat | tac | ttc | cca | ccc | cag | aag | acc | tgc | ctg | atc | tgt | gga | gat | gaa | 2766 | |
| Asp | Tyr | Tyr | Phe | Pro | Pro | Gln | Lys | Thr | Cys | Leu | Ile | Cys | Gly | Asp | Glu | | |
| | | | 535 | | | | 540 | | | | | 545 | | | | | |
| gct | tct | ggt | tgt | cac | tac | gga | gct | ctc | act | tgt | ggc | agc | tgc | aag | gtc | 2814 | |
| Ala | Ser | Gly | Cys | His | Tyr | Gly | Ala | Leu | Thr | Cys | Gly | Ser | Cys | Lys | Val | | |

Cont

| 550 | 555 | 560 | |
|---|-----|-----|------|
| ttc ttc aaa aga gct gcg gaa ggg aaa cag aag tat cta tgt gcc agc Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser 565 570 575 580 | | | 2862 |
| aga aat gat tgc acc att gat aaa ttt cgg agg aaa aat tgt cca tcg Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser 585 590 595 | | | 2910 |
| tgt cgt ctc cgg aaa tgt tat gaa gca ggg atg act ctg gga gct cgt Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg 600 605 610 | | | 2958 |
| aag ctg aag aaa ctt gga aat ctc aaa cta cag gaa gaa gga gaa aac Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu Asn 615 620 625 | | | 3006 |
| tcc agt gct ggt agc ccc act gag gac cca tcc cag aag atg act gta Ser Ser Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr Val 630 635 640 | | | 3054 |
| tca cac att gaa ggc tat gaa tgt caa cct atc ttt ctt aat gtc ctg Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val Leu 645 650 655 660 | | | 3102 |
| gaa gcc att gag cca gga gtg gtg tgt gcc gga cat gac aac aac cag Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn Gln 665 670 675 | | | 3150 |
| cct gat tcc ttt gct gcc ttg tta tct agt ctc aac gag ctt ggc gag Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu 680 685 690 | | | 3198 |
| aga cag ctt gta cat gtg gtc aag tgg gcc aag gcc ttg cct ggc ttc Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly Phe 695 700 705 | | | 3246 |
| cgc aac ttg cat gtg gat gac cag atg gca gtc att cag tat tcc tgg Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser Trp 710 715 720 | | | 3294 |
| atg gga ctg atg gta ttt gcc atg ggt tgg cgg tcc ttc act aat gtc Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn Val 725 730 735 740 | | | 3342 |
| aac tct agg atg ctc tac ttt gca cct gac ctg gtt ttc aat gag tat Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr 745 750 755 | | | 3390 |
| cgc atg cac aag tct cga atg tac agc cag tgc gtg agg atg agg cac Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg His 760 765 770 | | | 3438 |
| ctt tct caa gag ttt gga tgg ctc cag ata acc ccc cag gaa ttc ctg Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu 775 780 785 | | | 3486 |
| tgc atg aaa gca ctg cta ctc ttc agc att att cca gtg gat ggg ctg Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly Leu 790 795 800 | | | 3534 |

DI
Cont

aaa aat caa aaa ttc ttt gat gaa ctt cga atg aac tac atc aag gaa 3582
 Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu
 805 810 815 820

 ctt gat cgc atc att gca tgc aaa aga aaa aat ccc aca tcc tgc tca 3630
 Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser
 825 830 835

 agg cgc ttc tac cag ctc acc aag ctc ctg gat tct gtg cag cct att 3678
 Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile
 840 845 850

 gca aga gag ctg cat caa ttc act ttt gac ctg cta atc aag tcc cat 3726
 Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His
 855 860 865

 atg gtg agc gtg gac ttt cct gaa atg atg gca gag atc atc tct gtg 3774
 Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val
 870 875 880

 caa gtg ccc aag atc ctt tct ggg aaa gtc aag ccc atc tat ttc cac 3822
 Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His
 885 890 895 900

 aca cag tgaagatttg gaacctaata cccaaaccca cctgttccct ttccagatgt 3878
 Thr Gln

 cttctgacctg ttatataact ctgcactact tctctggcat gggccttggg ggaaattcct 3938
 ctactgatgt acagtctgtc atgaacatgt tccccagtt ctatttctctg ggcttttctc 3998
 tctttctttt tctttctctc tgcctctttt accctcccat ggcacatttt gaatccgctg 4058
 cgtgttggtg ctctgacctg tgttttgagt tttgttgat ttcttcaagt ctgtgatgat 4118
 cttcttggtg ccagtggtca actgtgcttg tttatagcac tgtgctgtgt gccaaccaag 4178
 caaatgttta ctaccttat gccatggcaa gtttagagag ctataagtat cttgggaaga 4238
 aacaaacaga gagagtaaaa aaaccaaaaa aaaaaaaaaa aaaccgaatt c 4289

<210> 21
 <211> 902
 <212> PRT
 <213> Rattus rattus

<400> 21

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1 5 10 15

Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20 25 30

Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile Ala
 35 40 45

Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
50 55 60

Arg Arg Arg Gln Gln His Pro Glu Asp Gly Ser Pro Gln Ala His Ile
65 70 75 80

Arg Gly Thr Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
85 90 95

Gln Gln Gln Ser Ala Ser Glu Gly His Pro Glu Ser Gly Cys Leu Pro
100 105 110

Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
115 120 125

Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
130 135 140

Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145 150 155 160

Lys Asp Ile Leu Ser Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
165 170 175

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
180 185 190

Gln Gln Gln Glu Val Ile Ser Glu Gly Ser Ser Ser Val Arg Ala Arg
195 200 205

Glu Ala Thr Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly
210 215 220

Asn Ser Thr Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser
225 230 235 240

Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly
245 250 255

Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro
260 265 270

Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly
275 280 285

Leu Ser Leu Asp Glu Gly Pro Gly Lys Gly Thr Glu Glu Thr Ala Glu
290 295 300

Tyr Ser Ser Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser
305 310 315 320

Leu Gly Cys Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu
325 330 335

Ile Pro Ser Ser Leu Ser Leu Tyr Lys Ser Gly Ala Val Asp Glu Ala
340 345 350

Ala Ala Tyr Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser
355 360 365

Gly Pro Pro His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys
370 375 380

Leu Glu Asn Pro Ser Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala
385 390 395 400

Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Gly Ser Val Ala
405 410 415

Gly Pro Ser Thr Gly Ser Pro Pro Ala Thr Ala Ser Ser Ser Trp His
420 425 430

Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly
435 440 445

Gly Gly Ser Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly
450 455 460

Tyr Thr Arg Pro Pro Gln Gly Leu Ala Ser Gln Glu Gly Asp Phe Ser
465 470 475 480

Ala Ser Glu Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr
485 490 495

Pro Ser Pro Ser Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn
500 505 510

Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His
515 520 525

Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile
530 535 540

Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly
545 550 555 560

Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr
565 570 575

Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys
580 585 590

Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr
595 600 605

Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu
610 615 620

Glu Gly Glu Asn Ser Ser Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln
625 630 635 640

Lys Met Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe
645 650 655

Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His
660 665 670

Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn
675 680 685

Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala
690 695 700

Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile
705 710 715 720

Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser
725 730 735

Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val
740 745 750

Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val
755 760 765

Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro

770

775

780

Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro
785 790 795 800

Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn
805 810 815

Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro
820 825 830

Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser
835 840 845

Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu
850 855 860

Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu
865 870 875 880

Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro
885 890 895

Ile Tyr Phe His Thr Gln
900

<210> 22
<211> 12
<212> DNA
<213> Artificial sequence

<220>
<223> Hypothetical oligonucleotide

<400> 22
gctgggttgta ag

12

<210> 23
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Hypothetical peptide

<400> 23

Ala Gly Cys Lys
1

<210> 24
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide probe A

<400> 24
cttttgaaga agaccttaca gccctcacag gt

32

<210> 25
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide probe B

<400> 25
ggaccatggt ttgcccatg actattactt tccacccc

38

<210> 26
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 26

Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr
1 5 10 15



TGCGTGAGGATGAGGCACCTTTCTCAAGAGTTTGGATGGCTCCAGATAACCCCCCAGGAA 3480
CysValArgMetArgHisLeuSerGlnGluPheGlyTrpLeuGlnIleThrProGlnGlu

TTCCTGTGCATGAAAGCACTGCTACTCTTCAGCATTATTCCAGTGGATGGGCTGAAAAAT 3540
PheLeuCysMetLysAlaLeuLeuLeuPheSerIleIleProValAspGlyLeuLysAsn

CAAAAATTCTTTGATGAACTTCGAATGAACTACATCAAGGAACTTGATCGCATCATTGCA 3600
GlnLysPhePheAspGluLeuArgMetAsnTyrIleLysGluLeuAspArgIleIleAla

TGCAAAAGAAAAAATCCCACATCCTGCTCAAGGCGCTTCTACCAGCTCACCAAGCTCCTG 3660
CysLysArgLysAsnProThrSerCysSerArgArgPheTyrGlnLeuThrLysLeuLeu

GATTCTGTGCAGCCTATTGCAAGAGAGCTGCATCAATTCACCTTTTGACCTGCTAATCAAG 3720
AspSerValGlnProIleAlaArgGluLeuHisGlnPheThrPheAspLeuLeuIleLys

TCCCATATGGTGAGCGTGGACTTTCCTGAAATGATGGCAGAGATCATCTCTGTGCAAGTG 3780
SerHisMetValSerValAspPheProGluMetMetAlaGluIleIleSerValGlnVal

CCCAAGATCCTTTCTGGGAAAGTCAAGCCCATCTATTTCCACACACAGTGAAGATTTGGA 3840
ProLysIleLeuSerGlyLysValLysProIleTyrPheHisThrGlnEnd

ACCTAATACCCAAACCCACCTGTTCCCTTTTCAGATGTCTTCTGCCTGTTATATAACTCT 3900

GCACTACTTCTCTGGCATGGGCCTTGGGGGAAATTCCTCTACTGATGTACAGTCTGTCAT 3960

GAACATGTTCCCAAGTTCTATTTCTGGGCTTTTCCTTCTTTCTTTTCTTCTTCTCTG 4020

CCTCTTTTACCCTCCCATGGCACATTTTGAATCCGCTGCGTGTTGTGGCTCCTGCCTGTG 4080

TTTTGAGTTTTGTTGTATTTCTTCAAGTCTGTGATGATCTTCTTGTGGCCCAGTGTCAAC 4140

TGTGCTTGTTTATAGCACTGTGCTGTGTGCCAACCAAGCAAATGTTTACTCACCTTATGC 4200

CATGGCAAGTTTAGAGAGCTATAAGTATCTTGGGAAGAAACAAACAGAGAGAGTAAAAAA 4260

ACCAAAAAAAAAAAAAAAAAAACCGAATTC 4289

FIG. 6D